

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/524,910  
Source: 10/524,910  
Date Processed by STIC: 2/26/05

# ***ENTERED***



PCT

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/524,910

DATE: 02/26/2005

TIME: 10:38:30

Input Set : A:\2543-1-040PCTUS - SEQUENCE LIST.txt

Output Set: N:\CRF4\02262005\J524910.raw

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3 <110> APPLICANT: TERRETT, JONATHAN A
6 <120> TITLE OF INVENTION: PTK7 PROTEIN INVOLVEMENT IN CARCINOMA
8 <130> FILE REFERENCE: 2543-1-040PCT/US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/524,910
C--> 12 <141> CURRENT FILING DATE: 2005-02-17
14 <150> PRIOR APPLICATION NUMBER: GB0219776.2
16 <151> PRIOR FILING DATE: 2002-08-24
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1070
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo Sapiens
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31 1 5 10 15
33 Leu Ser Val Leu Leu Leu Pro Leu Leu Gly Gly Thr Gln Thr Ala Ile
34 20 25 30
36 Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly Arg Arg
37 35 40 45
39 Ala Leu Leu Arg Cys Glu Val Glu Ala Pro Gly Pro Val His Val Tyr
40 50 55 60
42 Trp Leu Leu Asp Gly Ala Pro Val Gln Asp Thr Glu Arg Arg Phe Ala
43 65 70 75 80
45 Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln Asp Ser
46 85 90 95
48 Gly Thr Phe Gln Cys Val Ala Arg Asp Asp Val Thr Gly Glu Glu Ala
49 100 105 110
51 Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala Gly Pro
52 115 120 125
54 Val Val Leu Lys His Pro Ala Ser Glu Ala Glu Ile Gln Pro Gln Thr
55 130 135 140
57 Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro Thr Tyr
58 145 150 155 160
60 Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser Asn His
61 165 170 175
63 Thr Val Ser Ser Lys Glu Arg Asn Leu Thr Leu Arg Pro Ala Gly Pro
64 180 185 190
66 Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe Gly Gln
67 195 200 205
69 Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp Glu Ser Phe
70 210 215 220
72 Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg Tyr Glu

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73 225                230                235                240
75 Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro Ser Leu
76                245                250                255
78 Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser Arg Pro
79                260                265                270
81 Pro His Leu Arg Arg Ala Thr Val Phe Ala Asn Gly Ser Leu Leu Leu
82                275                280                285
84 Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile Gly Gln
85                290                295                300
87 Gly Gln Arg Gly Pro Pro Ile Ile Leu Glu Ala Thr Leu His Leu Ala
88 305                310                315                320
90 Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr Ala Gly
91                325                330                335
93 Ser Glu Glu Arg Val Thr Cys Leu Pro Pro Lys Gly Leu Pro Glu Pro
94                340                345                350
96 Ser Val Trp Trp Glu His Ala Gly Val Arg Leu Pro Thr His Gly Arg
97                355                360                365
99 Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala Glu Ser
100                370                375                380
102 Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly Gln Arg
103 385                390                395                400
105 Arg Gln Asp Val Asn Ile Thr Val Ala Thr Val Pro Ser Trp Leu Lys
106                405                410                415
108 Lys Pro Gln Asp Ser Gln Leu Glu Glu Gly Lys Pro Gly Tyr Leu Asp
109                420                425                430
111 Cys Leu Thr Gln Ala Thr Pro Lys Pro Thr Val Val Trp Tyr Arg Asn
112                435                440                445
114 Gln Met Leu Ile Ser Glu Asp Ser Arg Phe Glu Val Phe Lys Asn Gly
115                450                455                460
117 Thr Leu Arg Ile Asn Ser Val Glu Val Tyr Asp Gly Thr Trp Tyr Arg
118 465                470                475                480
120 Cys Met Ser Ser Thr Pro Ala Gly Ser Ile Glu Ala Gln Ala Arg Val
121                485                490                495
123 Gln Val Leu Glu Lys Leu Lys Phe Thr Pro Pro Pro Gln Pro Gln Gln
124                500                505                510
126 Cys Met Glu Phe Asp Lys Glu Ala Thr Val Pro Cys Ser Ala Thr Gly
127                515                520                525
129 Arg Glu Lys Pro Thr Ile Lys Trp Glu Arg Ala Asp Gly Ser Ser Leu
130                530                535                540
132 Pro Glu Trp Val Thr Asp Asn Ala Gly Thr Leu His Phe Ala Arg Val
133 545                550                555                560
135 Thr Arg Asp Asp Ala Gly Asn Tyr Thr Cys Ile Ala Ser Asn Gly Pro
136                565                570                575
138 Gln Gly Gln Ile Arg Ala His Val Gln Leu Thr Val Ala Val Phe Ile
139                580                585                590
141 Thr Phe Lys Val Glu Pro Glu Arg Thr Thr Val Tyr Gln Gly His Thr
142                595                600                605
144 Ala Leu Leu Gln Cys Glu Ala Gln Gly Asp Pro Lys Pro Leu Ile Gln
145                610                615                620

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```

147 Trp Lys Gly Lys Asp Arg Ile Leu Asp Pro Thr Lys Leu Gly Pro Arg
148 625                      630                      635                      640
150 Met His Ile Phe Gln Asn Gly Ser Leu Val Ile His Asp Val Ala Pro
151                      645                      650                      655
153 Glu Asp Ser Gly Arg Tyr Thr Cys Ile Ala Gly Asn Ser Cys Asn Ile
154                      660                      665                      670
156 Lys His Thr Glu Ala Pro Leu Tyr Val Val Asp Lys Pro Val Pro Glu
157                      675                      680                      685
159 Glu Ser Glu Gly Pro Gly Ser Pro Pro Pro Tyr Lys Met Ile Gln Thr
160                      690                      695                      700
162 Ile Gly Leu Ser Val Gly Ala Ala Val Ala Tyr Ile Ile Ala Val Leu
163 705                      710                      715                      720
165 Gly Leu Met Phe Tyr Cys Lys Lys Arg Cys Lys Ala Lys Arg Leu Gln
166                      725                      730                      735
168 Lys Gln Pro Glu Gly Glu Glu Pro Glu Met Glu Cys Leu Asn Gly Gly
169                      740                      745                      750
171 Pro Leu Gln Asn Gly Gln Pro Ser Ala Glu Ile Gln Glu Glu Val Ala
172                      755                      760                      765
174 Leu Thr Ser Leu Gly Ser Gly Pro Ala Ala Thr Asn Lys Arg His Ser
175                      770                      775                      780
177 Thr Ser Asp Lys Met His Phe Pro Arg Ser Ser Leu Gln Pro Ile Thr
178 785                      790                      795                      800
180 Thr Leu Gly Lys Ser Glu Phe Gly Glu Val Phe Leu Ala Lys Ala Gln
181                      805                      810                      815
183 Gly Leu Glu Glu Gly Val Ala Glu Thr Leu Val Leu Val Lys Ser Leu
184                      820                      825                      830
186 Gln Thr Lys Asp Glu Gln Gln Gln Leu Asp Phe Arg Arg Glu Leu Glu
187                      835                      840                      845
189 Met Phe Gly Lys Leu Asn His Ala Asn Val Val Arg Leu Leu Gly Leu
190                      850                      855                      860
192 Cys Arg Glu Ala Glu Pro His Tyr Met Val Leu Glu Tyr Val Asp Leu
193 865                      870                      875                      880
195 Gly Asp Leu Lys Gln Phe Leu Arg Ile Ser Lys Ser Lys Asp Glu Lys
196                      885                      890                      895
198 Leu Lys Ser Gln Pro Leu Ser Thr Lys Gln Lys Val Ala Leu Cys Thr
199                      900                      905                      910
201 Gln Val Ala Leu Gly Met Glu His Leu Ser Asn Asn Arg Phe Val His
202                      915                      920                      925
204 Lys Asp Leu Ala Ala Arg Asn Cys Leu Val Ser Ala Gln Arg Gln Val
205                      930                      935                      940
207 Lys Val Ser Ala Leu Gly Leu Ser Lys Asp Val Tyr Asn Ser Glu Tyr
208 945                      950                      955                      960
210 Tyr His Phe Arg Gln Ala Trp Val Pro Leu Arg Trp Met Ser Pro Glu
211                      965                      970                      975
213 Ala Ile Leu Glu Gly Asp Phe Ser Thr Lys Ser Asp Val Trp Ala Phe
214                      980                      985                      990
216 Gly Val Leu Met Trp Glu Val Phe Thr His Gly Glu Met Pro His Gly
217                      995                      1000                      1005
219 Gly Gln Ala Asp Asp Glu Val Leu Ala Asp Leu Gln Ala Gly Lys

```

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220      1010                      1015                      1020
222 Ala Arg  Leu Pro Gln Pro Glu  Gly Cys Pro Ser Lys  Leu Tyr Arg
223      1025                      1030                      1035
225 Leu Met  Gln Arg Cys Trp Ala  Leu Ser Pro Lys Asp  Arg Pro Ser
226      1040                      1045                      1050
228 Phe Ser  Glu Ile Ala Ser Ala  Leu Gly Asp Ser Thr  Val Asp Ser
229      1055                      1060                      1065
231 Lys Pro
232      1070
236 <210> SEQ ID NO: 2
237 <211> LENGTH: 4191
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo Sapiens
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243 cgggtgcgctc cgccctcctgt gcccgcgcgc gagcgcagtc tgcgcgcccg ccgtgcgccc 120
245 tcagctcctt ttcttgagcc cgccgcgatg ggagctgcgc ggggatcccc ggccagaccc 180
247 cgccggttgc ctctgctcag cgtcctgctg ctgccgctgc tgggcggtac ccagacagcc 240
249 attgtcttca tcaagcagcc gtctctccag gatgcactgc aggggcgcgc ggcgctgctt 300
251 cgctgtgagg ttgaggctcc gggcccggta catgtgtact ggctgctcga tggggccctt 360
253 gtccaggaca cggagcggcg ttctgcccag ggcagcagcc tgagctttgc agctgtggac 420
255 cggctgcagg actctggcac ctccagtggt gtggctcggg atgatgtcac tggagaagaa 480
257 gcccgcagtg ccaacgcctc ctccaacatc aaatggattg aggcaggtcc tgtgtgctg 540
259 aagcatccag cctcggaagc tgagatccag ccacagaccc aggtcacact tcgttgccac 600
261 attgatgggc accctcggcc cacctaccaaa tggttccgag atgggacccc cttttctgat 660
263 ggtcagagca accacacagt cagcagcaag gagcggaaacc tgacgctccg gccagctggt 720
265 cctgagcata gtgggctgta ttctgctgc gccacagtg cttttggcca ggcttgacgc 780
267 agccagaact tcaccttgag cattgctgat gaaagctttg ccagggtggt gctggcacc 840
269 caggacgtgg tagtagcgag gtatgaggag gccatgttcc attgccagtt ctacgcccag 900
271 cccccccga gctgcagtg gctctttgag gatgagactc ccatcactaa ccgagtcgc 960
273 cccccacacc tccgcagagc cacagtgttt gccaacgggt ctctgctgct gacccaggtc 1020
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277 atcctggaag ccacacttca cctagcagag attgaagaca tgccgctatt tgagccacgg 1140
279 gtgtttacag ctggcagcga ggagcgtgtg acctgccttc cccccaaggg tctgccagag 1200
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293 gaggtgtatg atgggacatg gtaccgttgt atgagcagca ccccagccgg cagcatcgag 1620
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301 gctgggaccc tgcattttgc ccgggtgact cgagatgacg ctggcaacta cacttgcat 1860
303 gctccaacg ggccgcaggg ccagattcgt gccatgtcc agctcactgt ggcagtttt 1920
305 atcaccttca aagtgaacc agagcgtacg actgtgtacc agggccacac agccctactg 1980
307 cagtgcgagg cccaagggga cccaagccg ctgattcagt ggaaaggcaa ggaccgcac 2040
309 ctggacccca ccaagctggg acccaggatg cacatcttcc agaatggctc cctggtgatc 2100

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311 catgacgtgg cccctgagga ctcaggccgc tacacctgca ttgcaggcaa cagctgcaac 2160
313 atcaagcaca cggaggcccc cctctatgtc gtggacaagc ctgtgccgga ggagtcggag 2220
315 ggccctggca gccctcccc ctacaagatg atccagacca ttgggttgct ggtgggtgcc 2280
317 gctgtggcct acatcattgc cgtgctgggc ctcatgttct actgcaagaa gcgctgcaaa 2340
319 gccaagcggc tgcagaagca gcccaggggc gaggagccag agatggaatg cctcaacggt 2400
321 gggcctttgc agaacgggca gccctcagca gagatccaag aagaagtggc cttgaccagc 2460
323 ttgggtccg gccccgcggc caccaacaaa cgccacagca caagtgataa gatgcacttc 2520
325 ccacggtcta gcctgcagcc catcaccacg ctggggaaga gtgagtttg ggaggtgttc 2580
327 ctggcaaagg ctcagggtt ggaggaggga gtggcagaga ccctggtact tgtgaagagc 2640
329 ctgcagagca aggatgagca gcagcagctg gacttccgga gggagttgga gatgtttggg 2700
331 aagctgaacc acgccaacgt ggtgcggctc ctggggctgt gccgggaggc tgagccccac 2760
333 tacatggtgc tgggaatatgt ggatctggga gacctcaagc agttcctgag gatttccaag 2820
335 agcaaggatg aaaaattgaa gtcacagccc ctcagcacca agcagaaggt ggccctatgc 2880
337 acccaggtag ccttgggcat ggagcacctg tccaacaacc gctttgtgca taaggacttg 2940
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345 ttcggtgtgc tgatgtggga agtgtttaca catggagaga tgcccatgg tgggcaggca 3180
347 gatgatgaag tactggcaga tttgcaggct gggaaggcta gacttctca gcccgagggc 3240
349 tgcccttcca aactctatcg gctgatgcag cgctgctggg ccctcagccc caaggaccgg 3300
351 ccctccttca gtgagattgc cagcgccctg ggagacagca ccgtggacag caagccgtga 3360
353 ggagggagcc cgctcaggat ggcctgggca ggggaggaca tctctagagg gaagctcaca 3420
355 gcatgatggg caagatccct gtcctcctgg gccctgaggc ccctgcccta gtgcaacagg 3480
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365 ctaggcttgg gatgagctgg gtttgtgggg agttccttaa tattctcaag ttctgggcac 3780
367 acagggttaa tgagtctctt cgcccactgg tcccacttgg gggctctagac caggattata 3840
369 gaggacacag caagtgagtc ctcccactc tgggcttggt cacactgacc cagacccacg 3900
371 tcttccccac ccttctctcc tttcctcatc ctaagtgcct ggcagatgaa ggagttttca 3960
373 ggagcttttg acactatata aaccgccctt tttgtatgca ccacgggcgg cttttatatg 4020
375 taattgcagc gtgggggtggg tgggcatggg aggtaggggt gggccctgga gatgaggagg 4080
377 gtgggccatc cttacccac acttttattg ttgtcgttt ttgtttgtt tgttttttg 4140
379 tttttgtttt tgtttttaca ctcgctgctc tcaataaata agcctttttt a 4191

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383 &lt;210&gt; SEQ ID NO: 3

384 &lt;211&gt; LENGTH: 22

385 &lt;212&gt; TYPE: DNA

386 &lt;213&gt; ORGANISM: Homo Sapiens

W--&gt; 387 &lt;400&gt; SEQUENCE: 3

388 cagccagaac ttcaccttga gc

22

392 &lt;210&gt; SEQ ID NO: 4

393 &lt;211&gt; LENGTH: 22

394 &lt;212&gt; TYPE: DNA

395 &lt;213&gt; ORGANISM: Homo Sapiens

W--&gt; 396 &lt;400&gt; SEQUENCE: 4

397 catgggagtc tcacctcaa ag

22

401 &lt;210&gt; SEQ ID NO: 5

402 &lt;211&gt; LENGTH: 14

**VERIFICATION SUMMARY**

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TIME: 10:38:31

Input Set : A:\2543-1-040PCTUS - SEQUENCE LIST.txt

Output Set: N:\CRF4\02262005\J524910.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:28 M:283 W: Missing Blank Line separator, <400> field identifier  
L:240 M:283 W: Missing Blank Line separator, <400> field identifier  
L:387 M:283 W: Missing Blank Line separator, <400> field identifier  
L:396 M:283 W: Missing Blank Line separator, <400> field identifier  
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